

hMOR-1A
Exon 3a ↓ **Exon 3b**
 ---ACTAATCATCAGGTACGCAGTCTCTAGAAATTAGGTATATCTACTGGGGATGACATAAAAAATTATAAGGCTT
 T N H Q V R S L * (SEQ ID NO:27)
 TGTGCTAAACTAGGAGTTTAATCCATTATAGAGGATGAGAATGGAGGGAAGAGGGGAAGCAAGGG (SEQ ID NO:28)

hMOR-1B1
Exon 3a ↓ **Exon 5a**
 ---ACTAATCATCAGAAAAATAGATTTATTCAAAAAGTCATCTTTACTCAACTGTGAGCATACCAAGGGCTAATA
 T N H Q K I D L F Q K S **S**[#] L L N C E H T K G * (SEQ ID NO:29)
 ATTACAATATTTTCCCGTGAAAGAAATATAAGATTGGAAGC (SEQ ID NO:30)

hMOR-1B2
Exon 3a ↓ **Exon 5b**
 ---ACTAATCATCAGAGAGAGAAAAGAACACAGAGAAATCTGACTGGTAAGAAATTGTACCTTTTGTCCAGCATGCCA
 T N H Q R E R Q K **S**[#] D W **S**[#] (SEQ ID NO:31)
 GGCTTCTGGGTTCCCTTTCCCTGAGCGGCCCTTAGTGATCCGGCTTGCGGCACCATCGCCTACGGGCC--- (SEQ ID NO:32)

hMOR-1B3
Exon 3a ↓ **Exon 5c**
 ---ACTAATCATCAGGGACCTCCAGCCAAAGTTTGTGTGACCAACTTGCCGGGTCGTCTTGAAAAAGGGGGCTT
 T N H Q G P P A K F V A D Q L A G S S * (SEQ ID NO:33)
 ACAGGTGTTCCAAAGCCCGTGTTTTATCCTGAAGTATCCCTCAACACACAGAAAAACGACCTCATAACACAAAA--- (SEQ ID NO:34)

hMOR-1B4
Exon 3a ↓ **Exon 5d**
 ---ACTAATCATCAGAGCTGACTATGACATGAACCCATAAAATTCCTGTTCCTCC--- (SEQ ID NO:35)
 T N H Q S * (SEQ ID NO:36)

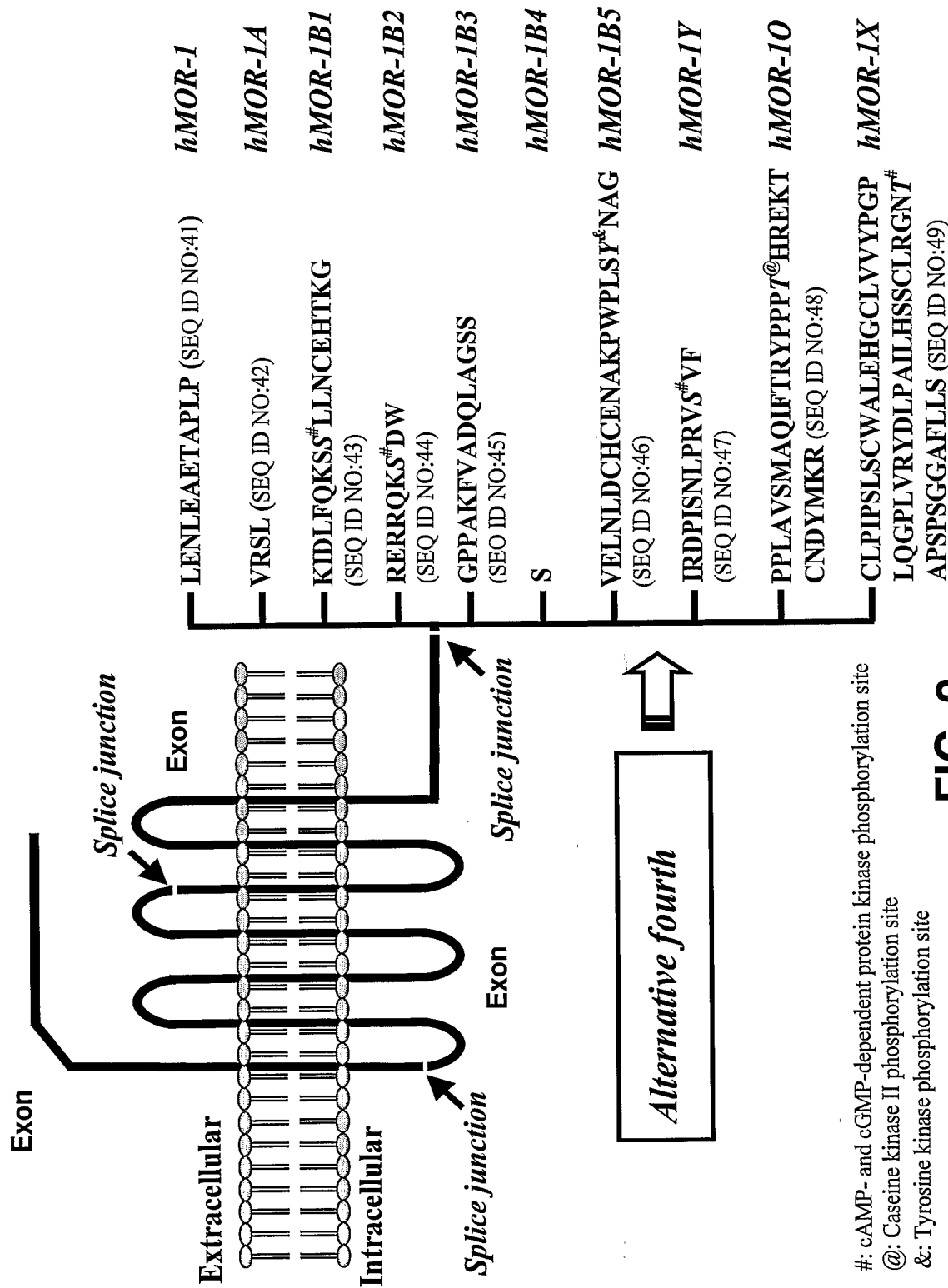
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FIG. 1B(1)

hMOR-1B5
Exon 3a ↓ Exon 5e
---ACTAATCATCAGGTGGAATTGAACCTGGACTGTCACTGTGAAAATGCAAGCCTTGGCCACTGAGCTACAA
T N H Q V E L N L D C H C E N A K P W P L S Y^e N
TGCAGGGTAGTCTCCATTTCCCTTCCAGGAAAGAGTCTAGAGCGTTA--- (SEQ ID NO:37)
A G * (SEQ ID NO:38)

hMOR-1Y
Exon 3a ↓ Exon Y
---ACTAATCATCAGATCAGAGATCCAATATCAAACTTCCAGGGTGTCTGTATTCTGACAACTGTCCACTGA
T N H Q I R D P I S N L P R V S[#] V F * (SEQ ID NO:39)
↓ Exon 5c
GGCAATTTCCATACAGCGCAAAAGTGGAGTGGCGATTGGCAGTTATCAAGGGACCTCCAGCCAAGTTTGTT--- (SEQ ID NO:40)

FIG. 1B(2)



#: cAMP- and cGMP-dependent protein kinase phosphorylation site
@: Caseine kinase II phosphorylation site
&: Tyrosine kinase phosphorylation site

FIG. 2

hMOR-1B2 (2218 bp)

CGGTGCTCCTGGCTACCTCGCACAGCGGTGCCCCGGCCGGTCAGTACCATGGACAGCAGCGCTGCCCCACGAAACG
 CCAGCAATTGCACCTGATGCCTTGGCGTACTCAAGTTGCTCCCCAGCACCCAGCCCGGTTCTTGGGTCAAATTGTCCCCA
 CTTAGATGGCAACCTGTCCGACCCATGCGGTCCGAACCGCACCGACTGGGCGGAGACAGCCTGTGCCCTCCGAC
 CGGCAGTCCCTCCATGATCACGGCCATCACGATCATGGCCCTCTACTCCATCGTGTGCGTGGGCTCTTCGGAAAC
 TTCCTGGTCATGTATGTGATTGTGAGATACACCAAGATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTCTGGC
 AGATGCCCTTAGCCACCAAGTACCCTGCCCTTCCAGAGTGTGAATTACCTAATGGGAACATGGCCATTGGAAACCATCCTT
 TGCAAGATAGTGATCTCCATAGATTACTATAACATGTTCAACCAAGCATATTCAACCTCTGCACCATGATGTTGATCGAT
 ACATTGCAGTCTGCCACCCCTGTCAAGGCCCTTAGATTTCGGTACTCCCGAAATGCCAAATTATCAATGTCTGCAACTG
 GATCCTCTCTTCAGCCATTGGTCTTCTGTAAATGTTTCATGGCTACAACAAATAACAGGCAAGGTTCCATAGATTGTACAC
 TAACATTCTCTCATCCAAACCTGTGACTGGGAAACCTGCTGAAGATCTGTGTTTTCATCTTCGCTTCATTATGCCAGTG
 CTCATCAATTACCGTGTGCTATGGAATGATCTTGGCCCTCAAGAGTGTCCGCATGCTCTGGCTCCAAAGAAAGG
 ACAGGAACTCTCGAAGGATCACAGGATGGTGTGGTGGTGTGCTGTGTTTCATCGTCTGGACTTCTGGCACTTCTGCACTGTCTAG
 TTACGTCATCAATTAAAGCCCTTGTTACAAATCCCAAGAACTACGTTCCAGACTGTTTCTGGCACTTCTGATGAGAGTTCTG
 GTTACACAAACAGCTGCCCTCAACCCAGTCTTTATGCAATTTCTGGATGAAACTTCAAAACGATGCTTCAGAGAGTTCTG
 TATCCCAACCTCTTCCAAACATTGAGCAACAAACTCCACTCGAATTCGTCAAGAACACTAGAGACCACCCCTCCACGGCC
 AATACAGTGGATAGAACTAATCATCAGAGAGAAAGAACAGAAATCTGACTGGTAAGAAATTGTACCCCTTTTGCCA
 GCATGCCAGGCTTCTGGGTTCCCTTTCCTGAGCGGCCCTAGTGATCCGGCTTGGCGCACCATCGCCTACGGGCCAAGC
 TGCATCATAAAGGAAATTTTCTTTTTCATTCTGGCCAGAGCAAAACACATGTGATAAAACATAGGCATTAGCTACTCTG
 CTTAGCACCAAATATCAGACTAGCTTAAATTTGCCCCAGATGGGTTCCATCATCTTTAATCCGACCTCTGACTTGCAGT
 TTCAACACGTGCTCTTTGGCAAAACAGTTGCCCTGAGTAACAGAAAGATAGGAAAGGAAAGGAGAGAGAGAA
 AATGTGCCCAGTGGAAAGGTGGGAAGGTGAAATGATCAAGGAGGCCAGAGAAAGACTCACCTATTGCAGCAACACT
 GTAGAAGTTCAGGCAGCTGCTTCTCGGTAGCAAAAGGATCTTTTCCAGCAATCCTATTAGCTCTCAAGTTTCCCCCTTTA
 GGGAGGAAAGCTCCCATGTCCCCGCAATCCTGTACATGTCCAAACCTTGCCAATCCACAGCCATCAGCAAGAGTGC
 AGACAGATTAAATCCAAAGAGAAATAGCAATTAATATCCCATAGCATCAAGCTGTCTTAGCCAAAGAGGACTTTAAACG
 GGAGGGTCTCTAACACCCCTAAATCTTAGAGAGACTCTAACCATCTTAAGTAGGGCTCTAACCCCGCTTTATAAACT
 TTTAATTGACTCCCATCTTAACAGTTGCAATCCATGGAGGAATGCTTGATAACCTCGGTGATAGATAAAAAACCAAGC
 ATACTAGAAAGTGTCTCTAAATTAATAATACAGTAGTTGCTAGAGAAATTTTGTCCAAATCCCAACTATAGAA
 ACATAGAAATGTGAGAGGTAGCACATAAGAAATAAGTCAATGGGATTTTATTTTCATGGACCAGCAATATGATGATAAAA
 GCCATCTAACCC (SEQ ID NO:52)

FIG. 3B(1)

hMOR-1B2 (397 aa)

MDSSAAPTNASNCITDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCPPTGSPSMITAITMALYSIVCVV
GLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDR
YIAVCHPVKALDERTPRNAKINVCNWLSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIIIV
CYGLMILRLKSVRMLSGSKEKDRNLRRIIRMLVVAVFIVCWTPHIIYVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPV
LYAFLDENFKRCFREFCIP TSSNIEQQNSTRIRQNTRDHPSTANTVDRTNHQRRRQKSDW
(SEQ ID NO:53)

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FIG. 3B(2)

hMOR-1B3 (2483 bp)

CGGTGCTCCTGGCTACCTCGCACAGCGGTGCCCGCCGGCCGTCAGTACCATGGACAGCAGCGGTGCCCCACGAAACG
 CCAGCAATTGCACACTGATGCCCTTGGCGTACTCAAGTTGCTCCCCAGCACCCAGCCCGGTTCTTGGGTCAAACCTTGTCCCA
 CTTAGATGGCAACCTGTCCGACCCATGCGGTCCGAACCGCACCGACCTGGGCGGAGAGACAGCCTGTGCCCTCCGAC
 CGGAGTCCCTCCATGATCAGGCCATACGATCATGGCCCTTACTCCATCGTGTGCGTGGGCTCTTCCGAAAC
 TTCTGTGTCATGTATGTGATGTGATGATACACCAAGATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTCTGGC
 AGATGCCCTTAGCCACCACTACCTGCCCTTCCAGAGTGTGAATTACCTAATGGGAACATGGCCATTGGAAACCATCCTT
 TGCAAGATAGTGTATCTCCATAGATTACTATAACATGTTCAACAGCATATTCAACCTCTGCAACCATGAGTGTGATCGAT
 ACATTGCAGTCTGCCACCCCTGTCAAGGCCCTTAGATTTCGGTACTCCCGAAATGCCAAATATCAATGTCTGCAACTG
 GATCCTCTCTTCAGCCATTGGTCTTCTGTAATGTTTCATGGCTACAAACAAATACAGGCAAGGTTCCATAGATTGTACAC
 TAACATTCTCTCATCCAACTGTGTAAGTGGAAACCTGCTGAAGATCTGTGTTTTCATCTTCGCCCTTCATTAATGCCAGTG
 CTCATCAATTACCGTGTGCTATGGAATGATCTTGGCCCTCAAGAGTGTCCGATGCTCTGTGGCTCCAAAGAAAGG
 ACAGGAATCTTCGAAGGATCACAGGATGTGTGTGGTGTGCTGTGTTCAATGCTGTGACTGCCATTCACAT
 TTACGTCAATCAATTAAGCCTTGGTTACAAATCCAGAACTACGTTCCAGACTGTTCTTGGCACTTCTGCAATGCTCTAG
 GTTACACAAACAGCTGCCCTAACCCAGTCTTTATGCAATTTCTGGATGAAAACCTTCAACGATGCTTCAGAGAGTTCTG
 TATCCCAACCTCTTCCAACTTGAGCAACAAACTCCACTCGAATTCGTCAAGAACTAGAGACCACCCCTCCACGGCC
 AATACAGTGGATAGAACTAATCATCAGGACCTCCAGCCAAAGTTTGTGTGCTGACCAACTTGGCCGGTCTGTGAAAGG
 GGGGCTTACAGGTGTTCCAAAGCCCGTGTTTTATCCTGAAGTATCCCTCAACACAGAAACAGACCTCATACACAAAT
 ACACCAAGCTTAAATAAGCCTTTGAATTAATTTTTCACATTAATCAAACTTTACAGAGGAGATAAACACTGATTTTAT
 TTTATTTTATTTTATTTTATTTTATTTTATTTGCAATTCATCAACCGTTTGACAGAGAGAAAGACAGAAATCTGACT
 GGTAAAGAAATTGTTACCTTTTGGCAGCATGCCAGGCTTCTGGGTTCCCTTTCCCTGAGCGGCCCTAGTGATCCGGCTTG
 CGGACCATCGCCTACGGGCCAAGCTGCATCATAAAGGAAATTTTATTTTTCATTTCTGGCCAGAGCAAAACACATGTGA
 TAAACATAGGCATTAGCTACTCTGCTTAGCACCAATAATCAGACTAGCTTAAATTTGCCCCAGACGGGTTCATCAT
 CTTTAAATCCGACCTCTGACTTGCAAGTTTCAACACGTGCTCTCTGGGCAAAACAGCTTGCCCTGAGTAACAGAAAGATAG
 GAAAGGAAAGGAGAGAGAGAAACCGTGCCAGTGGAAAGGTGGGAAAGGTGAATGATCAAGGAGGCCAGAGAAA
 GACTCACCTATTGCAGCAACACTGTAGAAGTTCAAGCAGCTGCTTCTCGGTAGCAAAAGGATCTTTTCCAGCAATCCTA
 TTAGCTCTCAAGTTTCCCTTTTAGGGAGGAAAGCTCCCATGTCCCGGATCTGTACATGTCCAAACCCCTGCCGTCC
 ACAGCCATCAGCAAGAGTGAAGACAGATTAAATCCAAAGAGAAATAGCGATTAAATATCCCATAGCATCAAAAGCTGTTT
 TTAGCCAAAGAGGACTTTAACGAGAGGGGTCTTAACACCCCTAAATCTTAGAAGAGACTCTAACCATCTTAAGTAGGG
 CCTCTAACCCCGCTTTATAAATTTAATTGACTCCCATCTTAACAGTTGCAATCCATGGAGGAATGCTTGATAACCTCG
 GTGATAAGATAAAACCAAGCATACTAGAAAGTGTCTCTAAATTAATAAATACAGTAGTTGTCTAGAGAAAAATTTTA

FIG. 3C(1)

GTCCAAAAATCCAACTATAGAAAACATAGAAATGTGAGAGGCAGCACATAAGAAAATAAGTCATGGGGATTTTATTTCAT
GGACCAAGCAATATGATGATAAAAGCCATCTAACC (SEQ ID NO:54)

hMOR-1B3 (403 aa)

MDSSAAPTNASNC'DALAYSSCSPAPSPGSWVNL'SHLDGNLSDPCGPNRTDLGGRDSLCPPTGSPSMITAITMALYSIVCVV
GLFGNFLVMYVIVRYTKMK'TATNIYFENLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNNMFTSIFTLCTMSVDR
YIAVCHPVKALDFRTPRNAKIINV'CNWILSSAIGLPVMMFMA'ATKYRQGSIDCTLTFSHPTWY'WENLLKICVFIFAFIMPVLIITV
CYGLMILRLKSVRMLSGSKEKDRNLRIRTRMV'LVVVAVFIVCWTPHIYVIAKALVTIPETTFQTVSWHFICIALGYTNSCLNPV
LYAFLDENFKRCFREFCIP'TSSNIEQQNSTRIRQNT'RDHPSTANTVDR'TNHQGP'PAKFVADQLAGSS (SEQ ID NO:55)

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FIG. 3C(2)

hMOR-1B4 (1251 bp)

CGGTGCTCCTGGCTACCTCGCACAGCGGTGCCCCGGCCGGTCACTACCATGGACAGCAGCGCTGCCCCACGAAACG
CCAGCAATTGCACCTGATGCCTTGGCGTACTCAAGTTGCTCCCGAGCACCCAGCCCCGGTTCTTGGTCAACTTGTCCCA
CTAGATGGCAACCTGTCCGACCCATCGGTCGAAACCGCACCGACCTGGGCGGAGAGACAGCCTGTGCCCCTCCGAC
CGCAGTCCCTCCATGATCACGGCCATCACGATCATGGCCCTCTACTCCATCGTGTGCGTGGTGGGCTCTTCGGAAAC
TTCTGGTCATGTATGTGATGTAGATACACCAAGATGAAGACTGCCACCAACATCTACGTTTTC AACCTTGTCTGGC
AGATGCCCTTAGCCACCAAGTACCTGCCCTTCCAGAGTGTGAATTACCTAATGGGAACATGGCCATTTGGAAACCATCCTT
TGCAAGATAGTGTCTCCATAGATTACTATAACATGTTCACCAAGCATAATTACCCCTCTGCACCATGAGTGTGATCGAT
ACATTGCAGTCTGCCACCCCTGTCAAGGCCTTAGATTTCGGTACTCCCGAAATGCCAAATTAATCAATGTCTGCAACTG
GATCCTCTCTCAGCCATTGGTCTTCCTGTAAATGTTTCATGGCTACAACAAAATACAGGCAAGGTTCCATAGATTGTACAC
TAACATTCTCTCATCCAAACCTGGTACTGGGAAAACCTGCTGAAGATCTGTGTTTTCATCTTCGCCCTTCATTATGCCAGTG
CTCATCATACCGTGTGCTATGGAAGTGTCTTGGCCCTCAAGAGTGTCCGCTCTCTCTGGTCCAAAGAAAAGG
ACAGGAATCTTCGAAGGATCACCAAGATGGTGTGGTGGTGTGTTTCATCGTCTGTGGACTCCCATTCACAT
TTACGTCAATCAATTAAGCCTTGGTTACAATCCAGAAACTACGTTCCAGACTGTTTCTTGGCACTTCTGCAATTGCTCTAG
GTTACACAAACAGCTGCCTCAACCCAGTCTTATGCATTTCTGGATGAAAACCTTCAACGATGCTTCAGAGAGTTCTG
TATCCCAACCTCTTCCAAACATTGAGCAACAAAACCTCCACTCGAATTCGTCAGAAACACTAGAGACCCCTCCACGGCC
AATACAGTGGATAGAACTAATCATCAGAGCTGACTATGACATGAACCCCTAAAATTCCTGTTCCTC (SEQ ID NO:56)

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hMOR-1B4 (389 aa)

MDSSAAPTNASNCTDALAYSSCAPSPGSWVNL SHLDGNLSDPCGPNRTDLGGRDSLCPPTGSPSMITAITMALYSIVCVV
GLFGNFLVMYVIVRYTKMKTATNIYVFENLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVD
RYIAVCHPVKALDFRTPRNAKIINV CNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWY WENLLKICVFIAFIMPVLIIT
VCYGLMILRLKSVRMLSGSKEKDRNLRRTRMVLVVAVFIVCWTPHIYVIKALVTIPETTFQIVSWHFCIALGYTNSCLNP
VL YAFLDENFKRCREFCIP TSSNIEQQNSTRI RQNTRDHPSTANTVDRTNHQS (SEQ ID NO:57)

FIG. 3D

hMOR-1B5 (1402 bp)

CGGTGCTCCTGGCTACCTCGCACAGCGGTGCCCGCCGGCGCTCAGTACCATGGACAGCAGCGCTGCCCCACGAAAG
CCAGCAATTGCACTGATGCCCTGGCGTACTCAAGTTGCTCCCGAGCACCCAGCCCCGGTTCCTGGGTCAACTTGTCCCA
CTTAGATGGCAACCTGTCCGACCCATGCGGTCCGAACCGCACCTGGCGGGAGAGACAGCCTGTGCCCTCCGAC
CGGCAGTCCCTCCATGATCACGGCCATCACGATCATGCCCCCTACTCCATCGTGTGCGTGTGGGCTCTTCGGAAAC
TTCCCTGGTCATGTATGTGATTGTGATACACCAAGATGAAGACTGCCACCAACATCTACATTTCAACCTTGCTCTGGC
AGATGCCCTTAGCCACAGTACCCTGCCCTTCAGAGTGTGAATTACCTAATGGGAACATGGCCATTTGGAAACCATCCTT
TGCAAGATAGTATCTCCATAGATTACTATAACATGTTCAACAGCATATTACCCCTCTGCACCATGAGTGTGATCGAT
ACATTGCAGTGTGCCACCTGTCAAGGCCTTAGATTTCCGTACTCCCCGAAATGCCAAATTAATCAATGTCTGCAACTG
GATCCTCTCTCAGCCATTGCTCTTCCGTAAATGTTCAATGGCTACAACAAATACAGGCAAGGTTCCATAGATTGTACAC
TAACATTCTCTCATCCAACTGGTACTGGGAAAACCTGCTGAAGATCTGTGTTTTCATCTTCGCCCTTCAATTATGCCAGTG
CTCATCATTAACCGTGTGCTATGGACTGATGATCTTGGCGCTCAAGAGTGTCCGCATGCTCTCTGGCTCCAAAGAAAAGG
ACAGGAATCTTCGAAGGATCACCAAGGATGGTGTGGTGTGCTGTGTTCAATCGTCTGTGGACTGTTCTTGGCACTTCTGCACTTGTCTAG
TTACGTCAATCAATAAGCCTTGGTTACAATCCAGAAACTACGTTCCAGACTGTTCTTGGCACTTCTGCACTTGTCTAG
GTTACACAAAACAGTGCCTCAACCCAGTCTTTATGCAATTTCTGGATGAAAACCTTCAACGATGCTTCAGAGAGTTCTG
TATCCCAACCTCTTCCAACATTGAGCAACAAAACCTCCACTCGAAATTCGTCAGAACACTAGAGACCAACCCCTCCACGGCC
AATACAGTGGATAGAACTAATCATCAGGTGGAATTGAACCTGGACTGCTACTGTGAAAATGCAAGCCTTGCCCACTG
AGCTACAAATGCAGGGTAGTCTCCATTTCCCTTCCAGGAAGAGTCTAGAGCGTTAATTTGAGTTTGGCGAAGGCTTGTA
ACTAATTCATATGATTTTAGAGCTGACTATGACATGAACCCCTAAAATTCCTGTTCCTC (SEQ ID NO:58)

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hMOR-1B5 (410 aa)

MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCPPTGSPSMITAITMALYSIVCVV
GLFGNFLVMYVIVRYTKMKTATNIYFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDR
YIAVCHPVKALDFRTPRNAKINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFFAFIMPVLIITV
CYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVVAVFIVCWTPHIYVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPV
LYAFLDENFKRCREFCIP TSSNIEQQNS TRIRQNTDRDHPSTANTVDRTNHQVELNLDCHCENAKPWPLSYNAG (SEQ ID
NO:59)

FIG. 3E

[illegible]

FIG. 3F(1)

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AGTTGCAATCCATGGAGGAATGCTTGATAACCTCGGTGATAAGATAAAAAACCAAGCATACTAGAGTGTCTCTCTAAA
ATTAAAAATACAGTAGTTGCTAGAGAAAAATTTTAGTCCAAAAATCCAACTATAGAAACATAGAAATGTGAGAGGTAGC
ACATAAGAAATAAGTCATGGGGATTTTATTTCATGGACCAGCAATATGATGATAAAAGCCATCTAACCAAGGGC
(SEQ ID NO:60)

hMOR-1Y (402 aa)

MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCPPTGSPSMITAITMALYSIVCVV
GLFGNFLVMYVIVRYTKMKTATNIYFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNNMFTSIFTLCTMSVDR
YIAVCHPVKALDFRTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLITV
CYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVFIVCWTPIHIVYIIKALVTIPETTFQTVSWHFCIALGYTNSCLNPV
LYAFLDENFKRCFREFCIPTSNIEQQNSTIRQNTRDHPSTANTVDRTNHQIRDPISNLP RVSVF (SEQ ID NO:61)

FIG. 3F(2)

hMOR-1 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSGWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1A (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSGWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1B1 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSGWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1B2 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSGWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1B3 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSGWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1B4 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSGWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1B5 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSGWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1O (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSGWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1X (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSGWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1Y (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSGWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
Consensus (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSGWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP

61

120

hMOR-1 (61) PTGSPSMITAITIMALYSIVCVWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1A (61) PTGSPSMITAITIMALYSIVCVWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1B1 (61) PTGSPSMITAITIMALYSIVCVWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1B2 (61) PTGSPSMITAITIMALYSIVCVWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1B3 (61) PTGSPSMITAITIMALYSIVCVWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1B4 (61) PTGSPSMITAITIMALYSIVCVWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1B5 (61) PTGSPSMITAITIMALYSIVCVWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1O (61) PTGSPSMITAITIMALYSIVCVWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1X (61) PTGSPSMITAITIMALYSIVCVWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1Y (61) PTGSPSMITAITIMALYSIVCVWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
Consensus (61) PTGSPSMITAITIMALYSIVCVWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT

FIG. 4(1)

121	180	
hMOR-1	(121)	STLPQSVNYLMGTWPFGTILCKIVISIDYNYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1A	(121)	STLPQSVNYLMGTWPFGTILCKIVISIDYNYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1B1	(121)	STLPQSVNYLMGTWPFGTILCKIVISIDYNYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1B2	(121)	STLPQSVNYLMGTWPFGTILCKIVISIDYNYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1B3	(121)	STLPQSVNYLMGTWPFGTILCKIVISIDYNYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1B4	(121)	STLPQSVNYLMGTWPFGTILCKIVISIDYNYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1B5	(121)	STLPQSVNYLMGTWPFGTILCKIVISIDYNYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1O	(121)	STLPQSVNYLMGTWPFGTILCKIVISIDYNYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1X	(121)	STLPQSVNYLMGTWPFGTILCKIVISIDYNYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1Y	(121)	STLPQSVNYLMGTWPFGTILCKIVISIDYNYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
Consensus	(121)	STLPQSVNYLMGTWPFGTILCKIVISIDYNYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
181	240	
hMOR-1	(181)	RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1A	(181)	RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1B1	(181)	RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1B2	(181)	RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1B3	(181)	RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1B4	(181)	RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1B5	(181)	RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1O	(181)	RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1X	(181)	RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1Y	(181)	RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
Consensus	(181)	RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI

FIG. 4(2)

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	300
hMOR-1	(241) FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVAVFIVCWTPIH
hMOR-1A	(241) FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVAVFIVCWTPIH
hMOR-1B1	(241) FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVAVFIVCWTPIH
hMOR-1B2	(241) FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVAVFIVCWTPIH
hMOR-1B3	(241) FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVAVFIVCWTPIH
hMOR-1B4	(241) FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVAVFIVCWTPIH
hMOR-1B5	(241) FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVAVFIVCWTPIH
hMOR-10	(241) FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVAVFIVCWTPIH
hMOR-1X	(241) FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVAVFIVCWTPIH
hMOR-1Y	(241) FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVAVFIVCWTPIH
Consensus	(241) FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVAVFIVCWTPIH
	360
hMOR-1	(301) YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSNI
hMOR-1A	(301) YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSNI
hMOR-1B1	(301) YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSNI
hMOR-1B2	(301) YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSNI
hMOR-1B3	(301) YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSNI
hMOR-1B4	(301) YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSNI
hMOR-1B5	(301) YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSNI
hMOR-10	(301) YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSNI
hMOR-1X	(301) YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSNI
hMOR-1Y	(301) YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSNI
Consensus	(301) YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSNI

FIG. 4(3)

361	420	
hMOR-1 (361)	EQQNSTRIRQNTRDHPSTANTVDRTNHQLENLEAETAPLP-----	
hMOR-1A (361)	EQQNSTRIRQNTRDHPSTANTVDRTNHQVRSL-----	
hMOR-1B1 (361)	EQQNSTRIRQNTRDHPSTANTVDRTNHQKIDLFQKSSLLNCEHTKG-----	
hMOR-1B2 (361)	EQQNSTRIRQNTRDHPSTANTVDRTNHQRRERQKSDW-----	
hMOR-1B3 (361)	EQQNSTRIRQNTRDHPSTANTVDRTNHQGPPAKFVADQLAGSS-----	
hMOR-1B4 (361)	EQQNSTRIRQNTRDHPSTANTVDRTNHQS-----	
hMOR-1B5 (361)	EQQNSTRIRQNTRDHPSTANTVDRTNHQVELNLDCHCENAKPWPLSYNAG-----	
hMOR-1O (361)	EQQNSTRIRQNTRDHPSTANTVDRTNHQPPPLAVSMAQIFTRYPPPTHREKTCNDYMKR--	
hMOR-1X (361)	EQQNSTRIRQNTRDHPSTANTVDRTNHQCPLPIPSLSCWALEHGCLVYYPGPLQGPLVRYD	
hMOR-1Y (361)	EQQNSTRIRQNTRDHPSTANTVDRTNHQIRDPISNLPVSVF-----	
Consensus (361)	EQQNSTRIRQNTRDHPSTANTVDRTNHQ	
421	446	
hMOR-1 (401)	----- (SEQ ID NO:62)	
hMOR-1A (393)	----- (SEQ ID NO:63)	
hMOR-1B1 (407)	----- (SEQ ID NO:51)	
hMOR-1B2 (398)	----- (SEQ ID NO:53)	
hMOR-1B3 (404)	----- (SEQ ID NO:55)	
hMOR-1B4 (390)	----- (SEQ ID NO:57)	
hMOR-1B5 (411)	----- (SEQ ID NO:59)	
hMOR-1O (419)	----- (SEQ ID NO:64)	
hMOR-1X (421)	LPAILHSSCLRGNTAPSPSGGAFLLS (SEQ ID NO:65)	
hMOR-1Y (403)	----- (SEQ ID NO:61)	
Consensus (388)	----- (SEQ ID NO:66)	

FIG. 4(4)

Exon 3a **↑** **Exon 3b**
 -----AACCAACAGGTATGTGCTTTCTAGAATTACGGATAACATATAAAAAATACCATATCTGGTA
 N H Q V C A F * (SEQ ID NO: 67)
 CCAGTCTAAGATTAAATCTTTAAGAAAGGTCAAGTAACTTGAGGCCAAAGTCC (SEQ ID NO: 68)

rMOR-1C1

Exon 3a ↓ **Exon 7**

-----AACCACCCAGCCCTGGCAGTCAGCGTGGCCAGATCTTTACAGGATATCCTTCTCCG
N H Q P A L A V S V A Q I F T G Y P S P

↓ **Exon 8**

ACTCATGTGAAAAACCCCTGCAAGAGTTACAGGGACAGACCTTAGACCCCTGTGGAAGAACGTGGT
T^d H G E K P C K **S^d** Y R D R P R P C G R T W
CTTTGAAATCGCGTGCAAGATCCAATGTGGAGCACITTCATTGTGGAGCCGCATTAATCTATAA
S^{c+} L K **S^d** R A E **S^d** N V E H F H C G A A L I Y N

↓ **Exon 9a**

CAATGTGAATTTTCATCTAAACACAGGGATGTGCTAGTGAGAAGTTTGGAGGTGCAGGC (SEQ ID NO:69)
N V N F I * (SEQ ID NO:70)

FIG. 5(1)

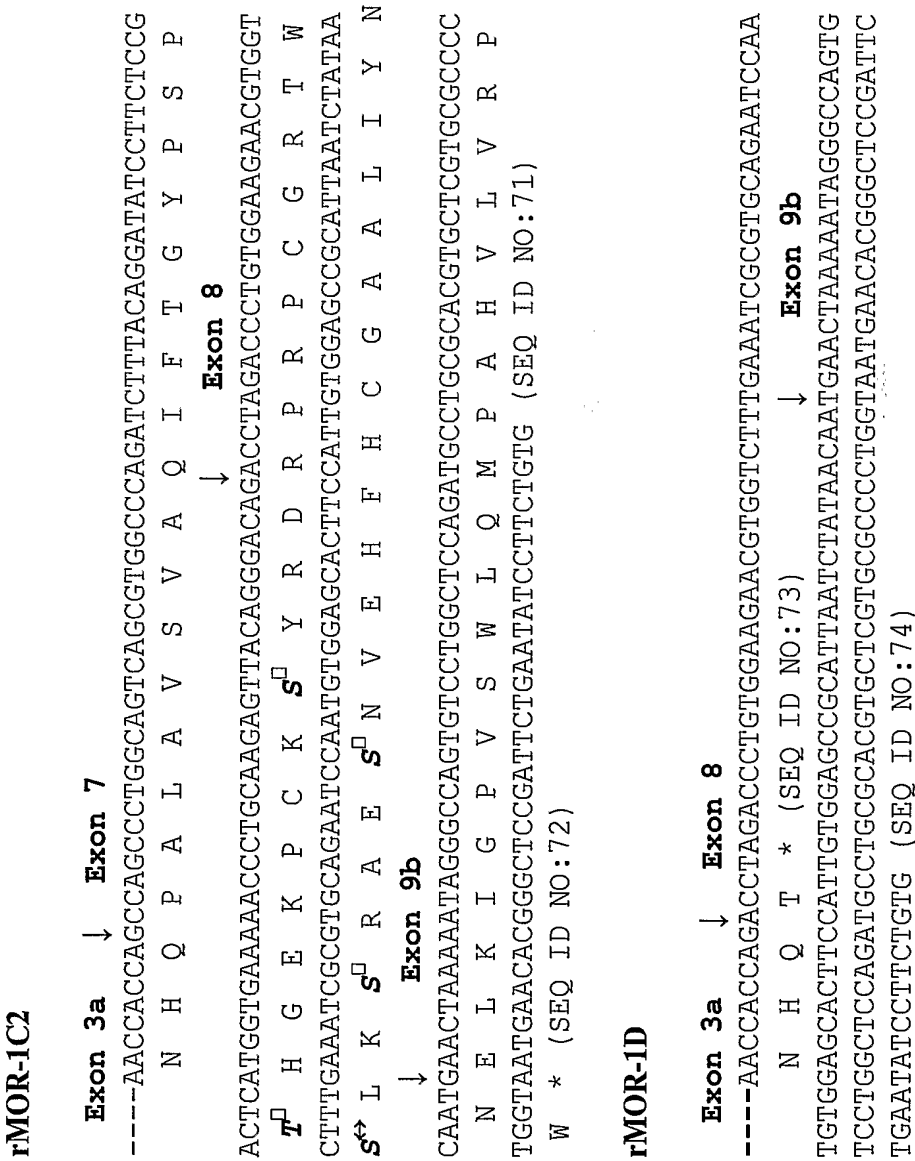


FIG. 5(2)

rMOR-1B2 (1628 bp)

GTTACAGCCTACCTAGTCCGCAGCAGGCCTTCAGCACCATGGACAGCAGCACCGGCCAGGGAACACACGCGACTGCT
CAGACCCCTTAGCTCAGGCAAGTTGCTCCCGCAGCACCTGGCTCCTGGCTCAACTTGTCCCACGTTGATGGCAACGAGTC
CGATCCATGCGGCTCTGAACCGCACCGGCTTGGCGGGAACGACAGCCTGTGCCCTCAGACCGGCAGCCCTTCCATGGT
CACAGCCATTACCATCATGGCCCTCTACTCTATCGTGTGTAGTGGGCTCTTCGGAACCTTCTCGTGGTCAATGTATGTGA
TTGTAAGATACACCAAAATGAAGACTGCCACCAACATCTACATTTCAACCTTGTCTGGCAGACGCTTAGCGACCAG
TACACTGCCCTTTTCAGAGTGTCAACTACCTGATGGGAACATGGCCCTTCGGAACCATCCTCTGCAAGATCGTGATTCA
ATAGATTACTACAACATGTTCAACGACATATTACCCCTCTGCACCATGAGCGTGGACCGCTACATTGCTGTCTGCCACC
CAGTCAAAAGCCCTGGATTTCCTACCCCGGAAATGCCAAATCGTCAACGCTGTGCAACTGGATCCTCTCTTCTGCCAT
CGGTCTGCCTGTAATGTTTCATGGCAACCAACAAATACAGGAGGGGTCCATAGATTGCACCTCACGTTCTCCACCCA
ACCTGGTACTGGGAGAACCTGCTCAAAATCTGTGCTTTATCTTCGCTTTCATCATGCGGTCCTCATCATCACTGTGTG
TTACGGCCTGATCTTACGACTCAAGAGCGTTCGCATGCTATCGGGCTCCAAAGAAAGGACAGGAAATTTGGCGCAG
GATCACCCGGATGGTGGTGGTGGTGTATTATCGTCTGTGACCCCATCCACATCTACGTCAATCAATAA
GCCTGATCACGATTCCAGAAACACATTTTCAGACCGTTTCCTGGCACTTCTGCATTTGCTTTGGTTACACGAACAGCT
GCCTGAATCCAGTCTTTTACGCTTCTGGGATGAAAACTTCAAGCGATGCTTCAGAAAGAGTTCTGCATCCCAACCTC
GTCCACGATCGAACAGCAAACTCCACTCGAGTCCGTCAGACACTAGGGAACATCCCTCCACGGCTAATACAGTGGA
TCGAACTAACCAACGAGCCTCAGTCAGTAGAGACATGATGTGAATGAACCAACTGATTAACAAGGTTTCTGAAC
ACTGAAATACAAACACAAATGTAGAGGTTACTAGAGAAATTTGTAGCCTGAAATTTCAATTACGGAAACCAATGAGT
GTGAGTGATACATTTTAAGGCCTCAGAGAGATTTTATTTTCATGACTAACAAACATGACCCAAAGCACCTAAACTGTGT
GATTAGATTACAAAGACAAATTTAGAGCCTGGGACTAAAGAAATGTTAGCCCTCACACAGACAGGCTCACACTTCAG
TAATGGAAATGAGCAATTAGATTAGTGAGAAAGATGGAGGAAAGACTCGAAATATTTTCATATCTTCTGTGGAACTC
CACAAAGAAACCAATAGAAATAAACCAACCTGTGGACCCCTTGGTGGCTCTTACC (SEQ ID NO:79)

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rMOR-1B2 (394 aa)

MDSSTGPNTSDCSDPLAQASCSPAGSWLNLSHVDGNQSDPCGLNRTGLGGNDSLCPQTGSPSMVTAITMALYSIVCVVG
LFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYNNMFTSIFTLCTMSVDY
IAVCHPVKALDFRTPRNAKIVNVCNWILSSAIGLPVFMFMAATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIITV
CYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVVAVFVVCWTPIHIYVIAKALITPETTFQTVSWHFCIALGYTNSCLNPVL
LRLPGMKTSSDASEEFCIPTSSSTIEQQNSTVRQNTREHPSTANTVDRTNHQEPQSVET (SEQ ID NO:80)

FIG. 6A

rMOR-1C1 (1433 bp)

GTACAGCCTACCTAGTCCGACGAGGCCTTCAGCACCATGACAGCAGCACCGGCCAGGAAACACAGCGACTGCT
CAGACCCCTTAGCTCAGGCAAGTTGCTCCCGACACCTGGCTCCTGGCTCAACTTGTCCACGTTGATGGCAACCCAGTC
CGATCCATGCGGTCTGAACCGCACCGGGCTTGGCGGGAACGACAGCCTGTGCCCTCAGACCGGCAAGCCCTTCCATGGT
CACAGCCATTACCATCATGCCCCCTACTCTATCGTGTGTAGTGGCCTCTTCGAAACTTCCTGGTCATGTATGTGA
TTGTAAGATACACCAAAATGAAGACTGCCACCAACATCTACATTTTCAACCTTGTCTGGCAGACGCCCTTAGCGACCCAG
TACACTGCCCTTTCAGAGTGTCAACTACTGATGGGAACATGGCCCTTCGGAACCATCCTCTGCAAGATCGTGATCTCA
ATAGATTACTAACATGTTACACAGCATATTCACCCCTCTGCACCATGAGCGTGGACCGCTACATTGCTGTCTGCCACC
CAGTCAAAGCCCTGGATTTCCGTACCCCCCGAAATGCCAAATCGTCAACGTCTGCAACTGGATCCTCTCTTCTGCCAT
CGGTCTGCCGTGTAATGTTTCATGGCAACCAACAATAACAGGAGGGGTCCATAGATTGCAACCCCTCACGTTCTCCACCCCA
ACCTGGTACTGGGAGAACCTGTCTCAAAATCTGTGTCTTTATCTTCGCTTTCATCATGCCGTCCTCATCATCACTGTGTG
TTACGGCCTGATGATCTTACGACTCAAAGCGTTCGCATGCTATCGGGCTCCAAAGAAAGGACAGGAATCTGCGCAG
GATCACCCGGATGGTGTGTCGTGCTGTAATTTATCGTCTGTGGACCCCATCCACATCTACGTCAATCATCAAA
GCGCTGATCACGATTCAGAAACCAATTCAGACCGTTTCTCGCACTTCTGCAATGCTTTGGGTTACACGAAACAGCT
GCCTGAAATCCAGTTCTTACGCCCTTCTGATGAAAACCTTCAAGCGATGCTTCAGAGAGTTCTGCATCCCAACCTCGTCC
ACGATCGAACAGCAAACTCCACTCGAGTCCGTCAGAACACTAGGGAACATCCCTCCACGGCTAATACAGTGGATCGA
ACTAACCCAGCCAGCCCTGGCAGTCAGCGTGGCCAGATCTTACAGGATATCCTTCTCCGACTCATGGTGAAAAAC
CCTGCAAGAGTTACAGGGACAGACCTAGACCCCTGTGGAAAGAACGTGGTCTTTTGAAATCGCGTGCAGAAATCCAAATGTGG
AGCACTTCCATTGTGGAGCCGCATTAATCTATAACAATGTGAATTTCACTAAACACAGGGATGTGCTAGTGAGAAAGTT
TGGAGGTGCAGGC (SEQ ID NO:81)

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rMOR-1C1 (451 aa)

MDSSTGPGNTSDCDPLAQASCSPAPGSWLNLSHVDGNQSDPCGLNRTGLGGNDSLCPQTGSPSMVTAITMALYSIVCVVG
LFGNFLVMYVIVRYTKMKTATNIYFNLAADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNNMFTSIFTLCTMSVDRY
IAVCHPVKALDFRTPRNAKIVNVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIITV
CYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVAVFIVCWTPHIVVIKALITIPETTFQTQVSWHFCIALGYTNSCLNPVL
YAFLDENFKRCREFCPTSSSTIEQQNSTVRQNTREHPSTANTVDRITNHQPALAVSVAQIFTGYPSPTHGEKPKCSYRDRPRP
CGRTWSLKSRAESNVEHFHCGAALIYNNVNF (SEQ ID NO:82)

FIG. 6B

rMOR-1C2 (1480 bp)

GTTACAGCCTACCTAGTCCGACGAGGCCTTTCAGCACCATGGACAGCAGCACGGCCACGGGAACACACGCGACTGCT
CAGACCCCTTAGCTCAGGCAAGTTGCTCCCCAGCACCTGGCTCCTGCTCAACTGTCCCACGTTGATGGCAACACAGTCC
CGATCCATGCGGTCTGAACGCAACGGGCTTGGCGGGAACGACAGCCTGTGCCCTCAGACCGGCAAGCCCTTCCATGGT
CACAGCCATTACCATCATATGGCCCTCTACTCTATCGTGTGTAGTGGCCTCTTCGGAACCTTCTCTGGTCAATGTATGTGA
TTGTAAGATACACCAAAATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTCTGGCAGACGCCCTTAGCGACCCAG
TACACTGCCCTTTTCAGAGTGTCAACTACCTGATGGGAACATGGCCCTTTCGGAACCATCTCTCTGCAAGATCGTGATCTCA
ATAGATTACTACAACATGTTCAACAGCATATTCAACCTCTGCAACCATGAGCGTGACCGCTACATTTGCTGTGCCACC
CAGTCAAAAGCCCTGGATTTCCGTACCCCCCGAAATGCCAAATCGTCAACGCTCTGCAACTGGATCCTCTCTCTGCCAT
CGGTCTGCCCTGTAATGTTTCATGGCAACCAACAAATACAGGCAAGGGTCCATAGATTGCACCCCTCACGTTCTCCACCCA
ACCTGGTACTGGGAGAACCTGCTCAAAATCTGTGCTTTATCTTCGCTTTCATCATGCGCGTCTCTCATCATCACTGTGTG
TTACGGCCTGATGATCTTACGACTCAAGAGCGTTCCGATGCTATCGGGCTCCAAAGAAAGGACAGGAATCTGCGCAG
GATCACCCGGATGGTGTGCTGTCGTGATTTATCGTCTGTGGACCCCATCCACATCTACGTCAATCATCAAA
GCGTGTACAGATTCCAGAAACCAATTTCAGACCGTTTCTTGGCACTTCTGCAATTGCTTTGGTTACACGAACAGCT
GCCTGAATCCAGTTCTTACGCTTCTGATGAAACTTCAAGCGATGCTTCAGAGAGTTCTGCATCCCAACCTCGTCC
ACGATCGAACACGAAACTCCACTCGAGTCCGTCAGAACACTAGGGAACATCCCTCCACGGCTAATACAGTGGATCGA
ACTAACCCAGCCAGCCCTGGCAGTCAGCGTGGCCAGATCTTTACAGGATATCCTTCTCCGACTCATGGTGAAAAAC
CCTGCAAGAGTTACAGGGACAGACCTAGACCTGTGGAAAGAACGTGGTCTTTTGAAATCGCGTGCAGAAATCCATGTGG
AGCACTTCCATTGTGGAGCCGCAATTAATCTATAACAATGAACATAAATAGGGCCAGTCTCTGGCTCCAGATGCCCTGC
GCACGTGCTCGTGGCCCCCTGGTAATGAACACGGGCTCCGATTCTGAATATCCTTCTGTG (SEQ ID NO:83)

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rMOR-1C2 (468 aa)

MDSSSTGPNGTSDCDPLAQASCSPAPGSWLNLSHVDGNQSDPCGLNRTGLGGNDLCPQTGSPSMVTAITMALYSIVCVVG
LFGNFLVMYVIVRYTKMKTATNIYFNALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFSTISFTLCTMSVDRY
IAVCHPVKALDFRTPRNAKIVNVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFFAFIMPVLIITV
CYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVVAVFVVCWTPIHIYVIKALITIPETTFQTVSWHFCIALGYTNSCLNPVL
YAFLDENFKRCFREFCIPTSSTIEQQNSTRVRQNTREHPSTANTVDRTNHQPALAVSVAQIFTGYPSPTHGEKPCCKSYDRPRP
CGRTWSLKSRAESNVEHFHCGAALIYNNELKIGPVSWLQMPAHVLVRPW (SEQ ID NO:84)

FIG. 6C

rMOR-1D (1385 bp)

GCCTACCTAGTCCGACGAGCCCTTCAGCACCATTGACACGACACCGGCCAGGAAACACGAGACTGCTCAGACC
 CCTTAGCTCAGGCAAGTTGCTCCCCAGCACCTGGCTCCTGGCTCAACTTGTCACCGTTGATGGCAACCAAGTCCGATCC
 ATCGGTCTGAACCGCACCGGGCTTGGGGAAACGACAGCCTGTGCCCTCAGACCGGACGCCCTTCCATGTCACAGC
 CATTACCATCATGGCCCTCTACTCTATCGTGTGTAGTGGCCCTCTTCGGAAACTTCCTGGTCATGTATGTGATTGTAA
 GATACACCAAAATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTCTGGCAGACGCCCTTAGCGACCACTACACT
 GCCCTTTCAGAGTGTCAACTACCTGATGGGAACATGGCCCTTCGGAAACCATCCTCTGCAAGATCGTGATCTCAATAGAT
 TACTACAAACATGTTACCCAGCATATTACCCCTCTGCACCATGAGCGTGGACCGCTACATTGCTGTCTGCCACCCAGTCA
 AAGCCCTGGATTTCGTACCCCGGAAATGCCAAATCGTCAACGTCTGCAACTGGATCCTCTCTTCTGCCATCGGTCT
 GCCTGTAATGTTTCATGGCAACCAACAAATACAGGACGGGTCCATAGATTGCACCCCTCACGTTCTCCCAACCCAAACCTGG
 TACTGGGAGAACCTGTCTCAAAATCTGTGTCTTGTCTTCGCTTTCATCATGCCGGTCCCTCATCATCACTGTGTGTACGG
 CCTGATGATCTTACGACTTAAGAGCTTCGATGCTATCGGGCTCCAAAGAAAGGACAGGAAATCTGCGCAGGATCAC
 CCGGATGGTGTGTGGTCTGTTATTCGCTGTGTGGACCCCTATCCACATCTACGTCAATCATCAAAAGCGCTG
 ATCAGGATTCAGAAACCAACATTTTCAGACCGTTTCTCGCACTTCTGCAATTGCTTTGGTTACACGAAACAGTGCCTGA
 ATCCAGTTCTTTACGCCCTTCTGGATGAAAACCTTCAAGCGATGCTTCAGAGAGTTCTGCATCCCAACCTCGTCCACGATC
 GAACAGCAAACTCCACTCGAGTCCGTCAGAACACTAGGGAACATCCCTCCACGGCTAATACAGTGGATCGAACTAAC
 CACCAGACCTAGACCTGTGGAAAGAACGTGGTCTTTGAAATCGCGTGCAGAAATCCAATGTGGAGCACTTCCATTGTGGA
 GCCGCATTAATCTATAACAAATGAACTAAATAGGGCCAGTGTCTCGCTCCAGATGCCCTGGCACGTCGTCTGTGCGCC
 CCTGGTAATGAACACGGGCTCCGATTCTGAATATCCTTCTGTG (SEQ ID NO:85)

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rMOR-1D (387 aa)

MDSSTGPGNTSDCDPLAQASCSPAPGSWLNLSHVDGNQSDPCGLNRTGLGGNDLCPQTGSPSMVTAITMALYSIVCVVG
 LFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFGLCKIVISIDYYNNMFTSIFTLCTMSVDRY
 IAVCHPVKALDFRTPRNAKIVNCNWILSSAIGLPVMFEMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFVFAFIMPVLITV
 CYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVFV/CWTPHIYVIAKALITPETTFQTVSWHFCIALGYTNSCLNPVL
 YAFLDENFKRCREFCIPTSSTIEQQNSTRVRQNTREHPSTANTVDRTNHQT (SEQ ID NO:86)

FIG. 6D

rMOR-1E (390 aa)

MDSSSTGPGNTSDCSDPLAQASCSPAPGSWLNLSHVDGNQSDPCGLNRTGLGGNDSLCPQTGSPSMVTAITMALYSIVCVVG
LFGNFLVMYVIVRYTKMKTATNIYENLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNNMFTSIFTLCTMSVDRY
IAVCHPVKALDFRTPRNAKIVNVCNWLSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLITV
CYGLMILRLKSVRMLSGSKEKDRNLRGITRMVLVVAVFIVCWTPIHYYVIKALITPETTFQTVSWHFCIALGYTNSCLNPVL
YAFLDENFKRCFREFCIPTSSTIEQQNSTRVQRNTREHPSTANTVDRTNHQGAEL (SEQ ID NO:88)

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FIG. 6E(2)